



US-107
SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> GENES INVOLVED IN POLYSACCHARIDE PRODUCTION AND
UTILIZATION THEREOF

<130> US-107

<150> JP 2003-32075

<151> 2003-02-10

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 1404

<212> DNA

<213> Methylophilus methylotrophus

<220>

<221> CDS

<222> (1)..(1404)

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Met	Val	Phe	Val	Leu	Trp	Gly	Leu	Phe	Ile	Tyr	Thr	Glu	Asn	Arg	Ile	
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Pro	Met	Ser	Ile	Phe	Ile	Thr	Ser	Ile	Val	Leu	Phe	Ser	Ile	Ser	Phe	
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ccc	agc	ggc	gcc	aag	att	cgc	aag	ggc	ttt	gcc	aag	atg	tgc	cgg	gat	240
Pro	Ser	Gly	Ala	Lys	Ile	Arg	Lys	Gly	Phe	Ala	Lys	Met	Cys	Arg	Asp	
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gtg	att	ggt	caa	tgg	ctg	gtc	att	gcc	acc	ttt	ttg	ctg	acc	ttt	gct	288
Val	Ile	Gly	Gln	Trp	Leu	Val	Ile	Ala	Thr	Phe	Leu	Leu	Thr	Phe	Ala	
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tat	atc	act	cgt	tac	atc	acc	tta	tat	agc	gaa	aaa	tta	att	ctc	gcc	336
Tyr	Ile	Thr	Arg	Tyr	Ile	Thr	Leu	Tyr	Ser	Glu	Lys	Leu	Ile	Leu	Ala	
			100					105					110			
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Trp	Leu	Ile	Val	Thr	Pro	Val	Ala	Gln	Ile	Ile	Ala	Leu	Gln	Leu	Leu	
		115					120					125				
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Lys	Trp	Ala	Ser	Pro	Lys	Leu	Ile	Glu	Trp	Gln	Gly	Pro	Arg	Gln	Asn	
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Thr	Leu	Ile	Ile	Gly	Leu	Asn	Glu	Gln	Gly	Leu	Leu	Leu	Ala	Asp	Asn	

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145																150																155																160	
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Leu	Lys	Arg	Asp	Tyr	Tyr	Gln	Arg	Ile	Asn	Ile	Leu	Gly	Phe	Phe	Glu																																		
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Phe	Ile	Asn	Val	Leu	Gln	Gly	Arg	Met	Ser	Val	Val	Gly	Pro	Arg	Pro																																		
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His	Ala	Val	Ala	His	Asn	Glu	Glu	Tyr	Arg	Lys	Leu	Ile	Lys	Gly	Tyr																																		
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atg	gta	cgc	cac	aag	gta	aaa	ccc	ggg	att	acc	ggc	tgg	gca	cag	gta	1248																																	
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Asn	Gly	Phe	Arg	Gly	Glu	Thr	Asp	Thr	Leu	Glu	Lys	Met	Glu	Gln	Arg																																		
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US-107

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 Gly Ala Tyr
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<213> Methylophilus methylotrophus

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 Pro Met Ser Ile Phe Ile Thr Ser Ile Val Leu Phe Ser Ile Ser Phe
 50 55 60
 Pro Ser Gly Ala Lys Ile Arg Lys Gly Phe Ala Lys Met Cys Arg Asp
 65 70 75 80
 Val Ile Gly Gln Trp Leu Val Ile Ala Thr Phe Leu Leu Thr Phe Ala
 85 90 95
 Tyr Ile Thr Arg Tyr Ile Thr Leu Tyr Ser Glu Lys Leu Ile Leu Ala
 100 105 110
 Trp Leu Ile Val Thr Pro Val Ala Gln Ile Ile Ala Leu Gln Leu Leu
 115 120 125
 Lys Trp Ala Ser Pro Lys Leu Ile Glu Trp Gln Gly Pro Arg Gln Asn
 130 135 140
 Thr Leu Ile Ile Gly Leu Asn Glu Gln Gly Leu Leu Leu Ala Asp Asn
 145 150 155 160
 Leu Lys Arg Asp Tyr Gln Arg Ile Asn Ile Leu Gly Phe Phe Glu
 165 170 175
 Asp Arg Ala Pro Asn Arg Leu Pro His Ile Asp Ser Tyr Pro Val Leu
 180 185 190
 Gly Ser Leu Asn Glu Leu Ser His Tyr Leu Lys Ser His Thr Val His
 195 200 205
 Lys Leu Tyr Ile Ala Leu Pro Met Ser Ser His Pro Arg Ile Leu Lys
 210 215 220
 Leu Leu Asp Asp Leu Lys Asp Thr Thr Ala Ser Ile Tyr Phe Val Pro
 225 230 235 240
 Asp Ile Phe Val Thr Asp Leu Ile Gln Gly Arg Val Ser Asp Val Asn
 245 250 255
 Gly Ile Pro Val Val Ser Val Cys Asp Thr Pro Phe Thr Gly Met Asp
 260 265 270
 Gly Phe Ile Lys Arg Thr Ala Asp Ile Leu Phe Ser Leu Leu Val Leu
 275 280 285
 Ile Leu Ile Ser Pro Ile Leu Ile Gly Ile Ala Ile Ala Val Lys Leu
 290 295 300
 Thr Ser Pro Gly Pro Val Ile Phe Lys Gln Arg Arg Tyr Gly Leu Asp
 305 310 315 320
 Gly Gln Gln Ile Leu Val Tyr Lys Phe Arg Ser Met Thr Val Thr Glu
 325 330 335

US-107

Asp Gly Ala Thr Val Thr Gln Ala Thr Arg Asn Asp Gln Arg Ile Thr
 340 345 350
 Pro Leu Gly Ala Phe Leu Arg Lys Thr Ser Leu Asp Glu Leu Pro Gln
 355 360 365
 Phe Ile Asn Val Leu Gln Gly Arg Met Ser Val Val Gly Pro Arg Pro
 370 375 380
 His Ala Val Ala His Asn Glu Glu Tyr Arg Lys Leu Ile Lys Gly Tyr
 385 390 395 400
 Met Val Arg His Lys Val Lys Pro Gly Ile Thr Gly Trp Ala Gln Val
 405 410 415
 Asn Gly Phe Arg Gly Glu Thr Asp Thr Leu Glu Lys Met Glu Gln Arg
 420 425 430
 Val His Tyr Asp Leu Glu Tyr Leu Arg Asn Trp Ser Pro Arg Leu Asp
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 Gly Ala Tyr
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 acg cga tta tgg ccg ttg tca cgc gcg gtt ttg cct aaa cag tta ttg 96
 Thr Arg Leu Trp Pro Leu Ser Arg Ala Val Leu Pro Lys Gln Leu Leu
 20 25 30
 cct ttg gtg acc gaa aat acg atg tta cag gag aca ttg atc cgg ctt 144
 Pro Leu Val Thr Glu Asn Thr Met Leu Gln Glu Thr Leu Ile Arg Leu
 35 40 45
 tct agc tgg gcg gat gtc ggt cat cct atc gtc gtc tgt ggt aac gat 192
 Ser Ser Trp Ala Asp Val Gly His Pro Ile Val Val Cys Gly Asn Asp
 50 55 60
 cat cgc ttt ttg gtg gcg gag caa tta cgg caa gtg aat ttg aca cct 240
 His Arg Phe Leu Val Ala Glu Gln Leu Arg Gln Val Asn Leu Thr Pro
 65 70 75 80
 gag gcg att gtg ctg gag ccg gtg gcg cga aat acg gca cct gcg att 288
 Glu Ala Ile Val Leu Glu Pro Val Ala Arg Asn Thr Ala Pro Ala Ile
 85 90 95
 gct gct gcg gct gtg act tta aaa gac aaa gat gtc ttg atg ctg gtg 336
 Ala Ala Ala Ala Val Thr Leu Lys Asp Lys Asp Val Leu Met Leu Val
 100 105 110
 ttg cct gcg gat cat gtg att act gac gtc act gct ttt gag gct gct 384
 Leu Pro Ala Asp His Val Ile Thr Asp Val Thr Ala Phe Glu Ala Ala
 115 120 125
 gtg cgt cgt gcc tgc gtt gca gca gag cag ggg aaa ctg gtc aca ttt 432
 Val Arg Arg Ala Cys Val Ala Ala Glu Gln Gly Lys Leu Val Thr Phe

US-107																
130	135	140														
ggt	ata	gag	cct	aca	cag	ccg	gaa	acc	ggt	tat	ggt	tat	atc	caa	tca	480
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Gly	Ala	Glu	Leu	Glu	Ala	Cys	Asp	Gly	Cys	Phe	Glu	Val	Ala	Arg	Phe	
				165					170					175		
ggt	gag	aag	cct	gat	gct	gcg	act	gca	cag	caa	tat	ttg	gat	gcc	gga	576
Val	Glu	Lys	Pro	Asp	Ala	Ala	Thr	Ala	Gln	Gln	Tyr	Leu	Asp	Ala	Gly	
			180					185					190			
aac	ttt	tat	tgg	aac	agc	ggc	atg	ttt	ttg	ttt	aaa	ccg	gct	gtg	ttc	624
Asn	Phe	Tyr	Trp	Asn	Ser	Gly	Met	Phe	Leu	Phe	Lys	Pro	Ala	Val	Phe	
			195				200					205				
ctg	gct	gag	ttg	cag	caa	tac	gcg	cca	gcc	atg	gtc	agt	gcg	gta	agc	672
Leu	Ala	Glu	Leu	Gln	Gln	Tyr	Ala	Pro	Ala	Met	Val	Ser	Ala	Val	Ser	
	210					215					220					
aat	gcc	ggt	gcg	caa	agt	tat	aaa	gac	ctg	gat	ttt	gtg	cgc	ttg	cat	720
Asn	Ala	Val	Ala	Gln	Ser	Tyr	Lys	Asp	Leu	Asp	Phe	Val	Arg	Leu	His	
225					230				235					240		
gag	gcc	tcg	ttt	gct	gag	tct	cct	tct	gat	tca	att	gac	tat	gcc	gtc	768
Glu	Ala	Ser	Phe	Ala	Glu	Ser	Pro	Ser	Asp	Ser	Ile	Asp	Tyr	Ala	Val	
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atg	gaa	aaa	acc	aaa	ctg	gcg	gcc	gtg	gta	cct	gcc	agc	atg	ggg	tggt	816
Met	Glu	Lys	Thr	Lys	Leu	Ala	Ala	Val	Val	Pro	Ala	Ser	Met	Gly	Trp	
			260					265					270			
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gcg	gat	ggg	aat	gct	aca	cggt	ggg	gat	gtg	ttt	ctt	aaa	aat	gtg	aaa	912
Ala	Asp	Gly	Asn	Ala	Thr	Arg	Gly	Asp	Val	Phe	Leu	Lys	Asn	Val	Lys	
290						295					300					
aat	acc	ttg	gta	cggt	gcgt	gaa	gag	cggt	ttt	gtg	gct	gcc	ggt	ggc	gta	960
Asn	Thr	Leu	Val	Arg	Ala	Glu	Glu	Arg	Phe	Val	Ala	Ala	Val	Gly	Val	
305					310				315						320	
gag	gat	ttg	ctg	att	ggt	gaa	acc	agt	gat	gcgt	atc	ctg	ggt	gcgt	cac	1008
Glu	Asp	Leu	Leu	Ile	Val	Glu	Thr	Ser	Asp	Ala	Ile	Leu	Val	Ala	His	
				325					330					335		
cgt	gat	tgt	gcgt	cag	gat	gtc	aag	aat	att	ggt	gat	cat	ttg	aag	gca	1056
Arg	Asp	Cys	Ala	Gln	Asp	Val	Lys	Asn	Ile	Val	Asp	His	Leu	Lys	Ala	
			340					345					350			
agc	gga	cgt	tct	gaa	cat	aag	atg	cat	ccc	cgt	ggt	tat	cgc	cct	tggt	1104
Ser	Gly	Arg	Ser	Glu	His	Lys	Met	His	Pro	Arg	Val	Tyr	Arg	Pro	Trp	
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ggt	tggt	tac	gag	gga	atc	gat	atc	ggc	gag	cgt	ttc	cag	gtc	aag	cgt	1152
Gly	Trp	Tyr	Glu	Gly	Ile	Asp	Ile	Gly	Glu	Arg	Phe	Gln	Val	Lys	Arg	
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Ile	Met	Val	Lys	Pro	Gly	Glu	Arg	Leu	Ser	Leu	Gln	Met	His	His	His	
385					390				395						400	
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Arg	Ala	Glu	His	Trp	Val	Val	Val	Ser	Gly	Ala	Met	Ile	Thr	Ile		
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gat	gat	gtc	acc	aag	ctc	tat	act	gaa	aac	gaa	tct	act	tat	ata	ccgt	1296
Asp	Asp	Val	Thr	Lys	Leu	Tyr	Thr	Glu	Asn	Glu	Ser	Thr	Tyr	Ile	Pro	
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US-107

att ggc tca acg cac cga cta gag aat cca ggt aaa ttg cct ttg cat	1344
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435 440 445	
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Leu Ile Glu Val Gln Ser Gly Ser Tyr Leu Gly Glu Asp Asp Ile Val	
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<213> Methylophilus methylotrophus

<400> 4

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Ser Ser Trp Ala Asp Val Gly His Pro Ile Val Val Cys Gly Asn Asp	
50 55 60	
His Arg Phe Leu Val Ala Glu Gln Leu Arg Gln Val Asn Leu Thr Pro	
65 70 75 80	
Glu Ala Ile Val Leu Glu Pro Val Ala Arg Asn Thr Ala Pro Ala Ile	
85 90 95	
Ala Ala Ala Ala Val Thr Leu Lys Asp Lys Asp Val Leu Met Leu Val	
100 105 110	
Leu Pro Ala Asp His Val Ile Thr Asp Val Thr Ala Phe Glu Ala Ala	
115 120 125	
Val Arg Arg Ala Cys Val Ala Ala Glu Gln Gly Lys Leu Val Thr Phe	
130 135 140	
Gly Ile Glu Pro Thr Gln Pro Glu Thr Gly Tyr Gly Tyr Ile Gln Ser	
145 150 155 160	
Gly Ala Glu Leu Glu Ala Cys Asp Gly Cys Phe Glu Val Ala Arg Phe	
165 170 175	
Val Glu Lys Pro Asp Ala Ala Thr Ala Gln Gln Tyr Leu Asp Ala Gly	
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Asn Phe Tyr Trp Asn Ser Gly Met Phe Leu Phe Lys Pro Ala Val Phe	
195 200 205	
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Asn Ala Val Ala Gln Ser Tyr Lys Asp Leu Asp Phe Val Arg Leu His	
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Met Glu Lys Thr Lys Leu Ala Ala Val Val Pro Ala Ser Met Gly Trp	
260 265 270	
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275 280 285	
Ala Asp Gly Asn Ala Thr Arg Gly Asp Val Phe Leu Lys Asn Val Lys	
290 295 300	
Asn Thr Leu Val Arg Ala Glu Glu Arg Phe Val Ala Ala Val Gly Val	

US-107

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Arg	Asp	Cys	Ala	Gln	Asp	Val	Lys	Asn	Ile	Val	Asp	His	Leu	Lys	Ala	
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Ser	Gly	Arg	Ser	Glu	His	Lys	Met	His	Pro	Arg	Val	Tyr	Arg	Pro	Trp	
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Gly	Trp	Tyr	Glu	Gly	Ile	Asp	Ile	Gly	Glu	Arg	Phe	Gln	Val	Lys	Arg	
	370					375					380					
Ile	Met	Val	Lys	Pro	Gly	Glu	Arg	Leu	Ser	Leu	Gln	Met	His	His	His	
	385				390					395					400	
Arg	Ala	Glu	His	Trp	Val	Val	Val	Ser	Gly	Ser	Ala	Met	Ile	Thr	Ile	
				405					410					415		
Asp	Asp	Val	Thr	Lys	Leu	Tyr	Thr	Glu	Asn	Glu	Ser	Thr	Tyr	Ile	Pro	
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Ile	Gly	Ser	Thr	His	Arg	Leu	Glu	Asn	Pro	Gly	Lys	Leu	Pro	Leu	His	
		435					440					445				
Leu	Ile	Glu	Val	Gln	Ser	Gly	Ser	Tyr	Leu	Gly	Glu	Asp	Asp	Ile	Val	
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<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer Km4-R2

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accaacgcgt aatcgcccca tcatccagcc agaaagtga 39

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer Km4-R1

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<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer mManC-F1

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<210> 11
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<220>
<223> Description of Artificial Sequence: primer mManC-R1

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<210> 12
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<212> DNA
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<220>
<223> Description of Artificial Sequence: primer mManC-F2

<400> 12
atttgaggtc ggtttgcttg cgctatttta acg 33

US-107

<210> 13

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer mManC-R2

<400> 13

tcgtgacata gcgttgacaca tagccctcat a

31